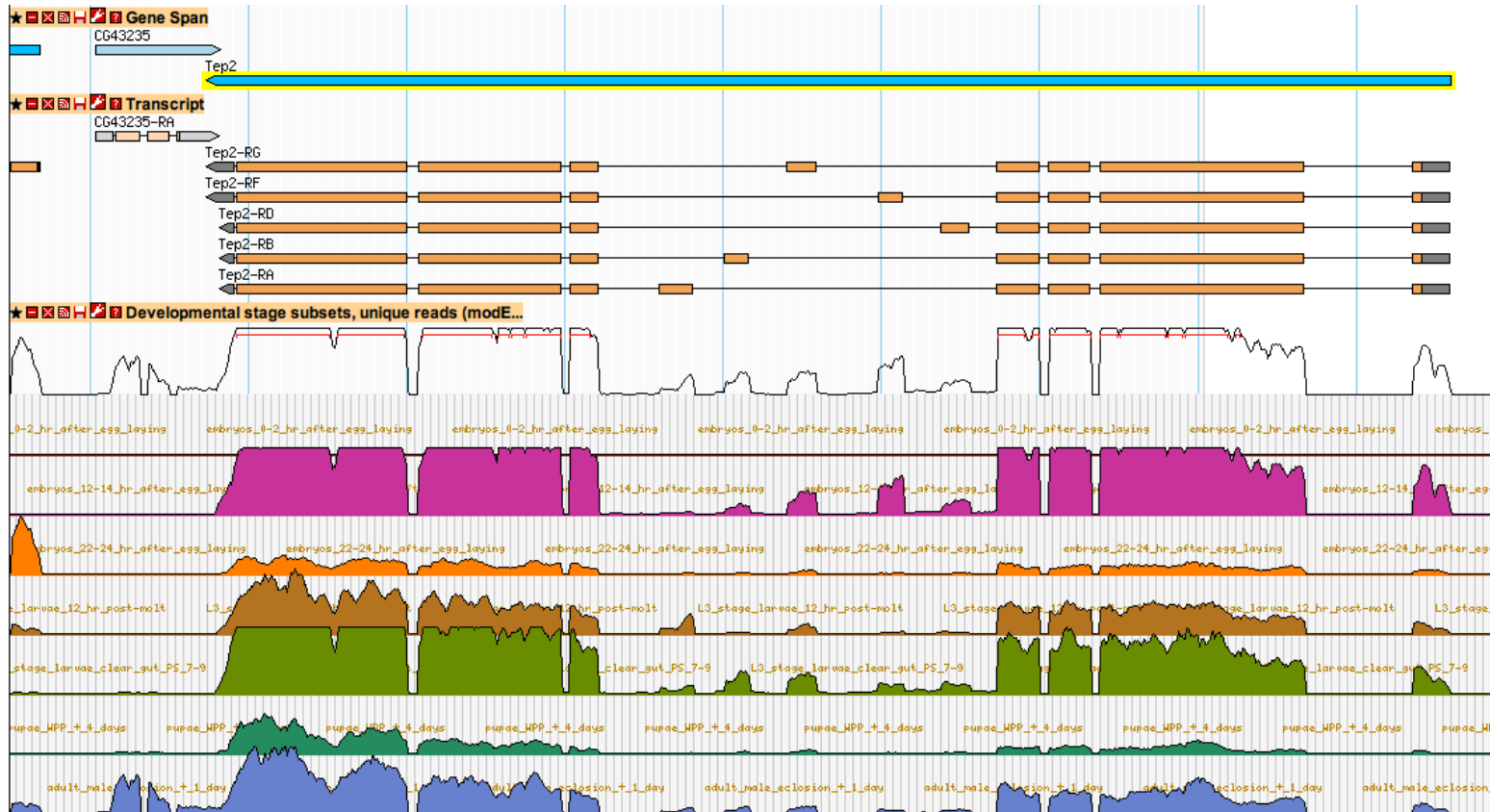




New views in GBrowse2:

Release 6 *D. melanogaster* assembly, RNA-Seq data, and more

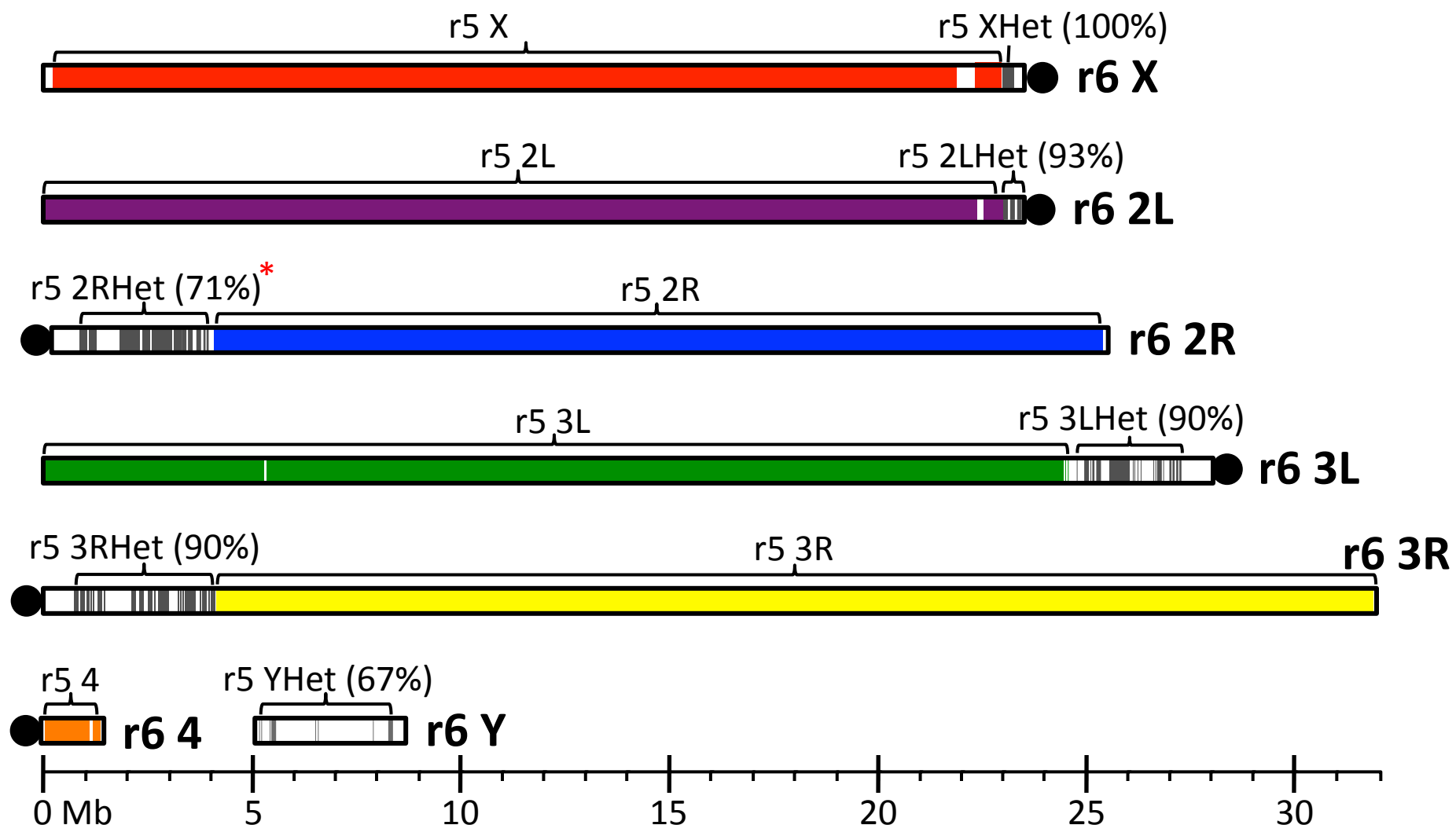


The Release 6 reference sequence of the *Drosophila melanogaster* genome

Roger A. Hoskins,¹ Joseph W. Carlson,^{1,10} Kenneth H. Wan,¹ Soo Park,¹ Ivonne Mendez,¹ Samuel E. Galle,¹ Benjamin W. Booth,¹ Barret D. Pfeiffer,² Reed A. George,² Robert Svirskas,² Martin Krzywinski,³ Jacqueline Schein,³ Maria Carmela Accardo,⁴ Elisabetta Damia,⁴ Giovanni Messina,⁴ María Méndez-Lago,⁵ Beatriz de Pablos,⁵ Olga V. Demakova,⁶ Evgeniya N. Andreyeva,⁶ Lidiya V. Boldyreva,⁶ Marco Marra,³ A. Bernardo Carvalho,⁷ Patrizio Dimitri,⁴ Alfredo Villasante,⁵ Igor F. Zhimulev,^{6,8} Gerald M. Rubin,² Gary H. Karpen,^{1,9} and Susan E. Celniker¹

- Improvement to centric heterochromatin regions.
- Improved Y chromosome assembly (now 10 times larger).

Release 5 - Release 6 comparison



*% of r5 'Het' mapped to r6 arm assembly indicated.

Depiction *approximates* NCBI Release 5-to-Release 6 Alignment

Most feature coordinates have changed.

Release 5 region*	Release 6 coordinates	size (Mb)	shift (bp)
X:4,684,795..20,073,489	X:4,790,762..20,179,456	15.4	105,967
2L:1..21,485,538	2L:1..21,485,538	21.4	0
2R:3,037..16,668,212	2R:4,115,532..20,780,707	16.7	4,112,495
3L:5,114,766..24,523,740	3L:5,121,666..24,530,640	24.5	6,900
3R:1..27,905,053	3R:4,174,279..32,079,331	27.9	4,174,278
4:24,054..1,221,288	4:3,428..1,200,662	1.2	20,626

*For each Release 6 chromosome arm assembly, the largest region of uninterrupted identity from Release 5 is shown.

A complete liftover table is available at <http://flybase.org/reports/FBrf0225389.html>

Mapping of Release 5 sequences to Release 6: pseudoscaffold U is no more

- 24% of r5 **U** sequence has moved onto the r6 chromosome arm assemblies:
 - X – 223 kb
 - 2L – 40 kb
 - 2R – 994 kb
 - 3L – 150 kb
 - 3R – 1,027 kb
- 1,862 minor scaffolds remain as distinct entities (not a pseudoscaffold).
- About half of the minor scaffolds have been mapped cytologically:
 - e.g., 2CEN, 3CEN, rDNA, Y.

Migration of FlyBase features to Release 6

- The vast majority of FlyBase features migrated automatically, using mapping table derived from NCBI genome alignment.
- 77 gene models required manual review.
 - 31 gene models were deleted (non-coding repeats)
 - 13 gene models had protein coding changes.
 - 33 mapped to the new assembly without major changes.
- 11 new gene models were assembled from 40 annotation fragments due to improvements in centric heterochromatin.

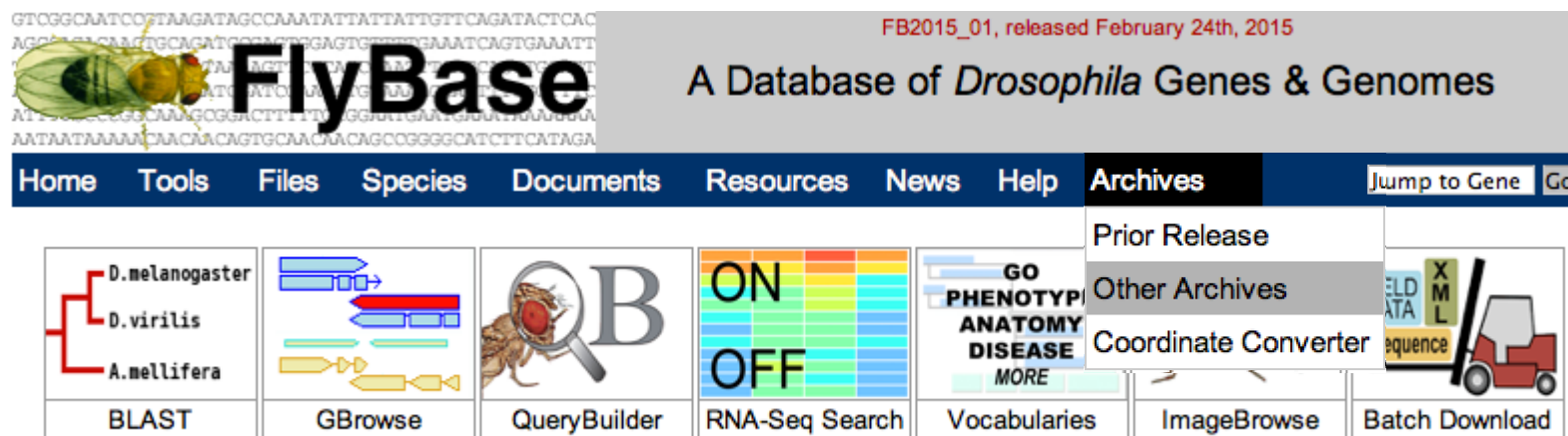
See the current release notes for full details of affected genes.

http://flybase.org/static_pages/docs/release_notes.html

Migration of FlyBase evidence to Release 6

- NCBI has provided new alignments of nucleotide and protein sequences.
- Sue Celniker's group has provided modENCODE RNA-Seq data newly mapped to the Release 6 assembly.
- Other RNA-Seq data has been migrated by FlyBase.

Access to Release 5 data: FlyBase Archives



The image shows the FlyBase website header and navigation menu. The header includes the FlyBase logo, a fly illustration, and the text "FlyBase A Database of *Drosophila* Genes & Genomes". The navigation menu includes "Home", "Tools", "Files", "Species", "Documents", "Resources", "News", "Help", and "Archives". The "Archives" menu is open, showing options like "Prior Release", "Other Archives", and "Coordinate Converter".

FB2015_01, released February 24th, 2015

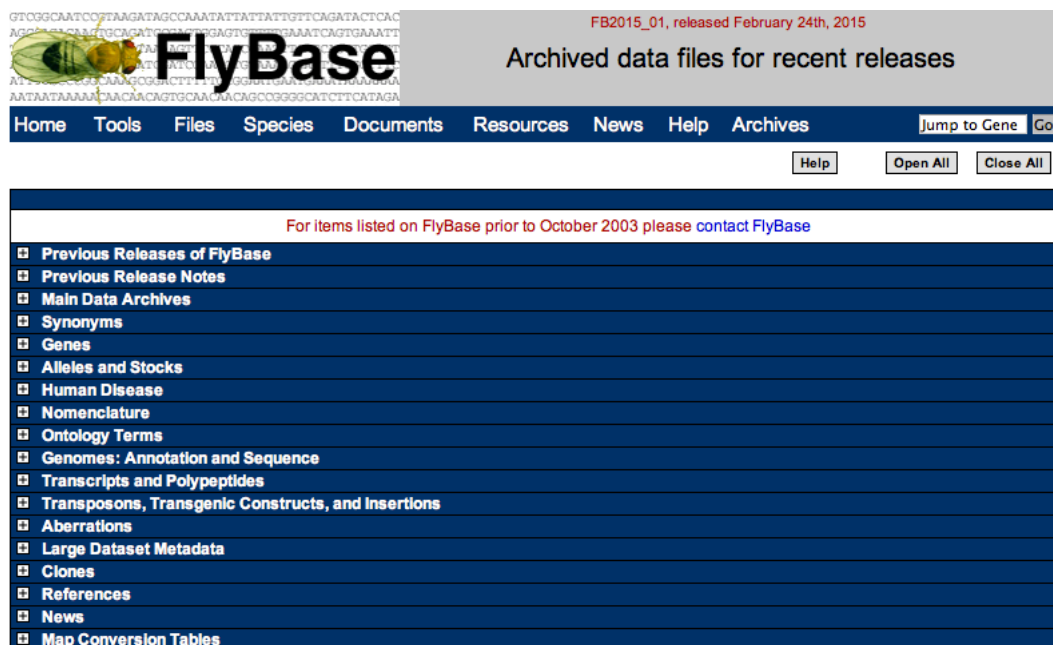
FlyBase A Database of *Drosophila* Genes & Genomes

Home Tools Files Species Documents Resources News Help Archives Jump to Gene Go

Prior Release
Other Archives
Coordinate Converter

BLAST GBrowse QueryBuilder RNA-Seq Search Vocabularies ImageBrowse Batch Download

http://flybase.org/static_pages/downloads/archivedata3.html



The image shows the FlyBase website header and a list of archived data files for recent releases. The header includes the FlyBase logo, a fly illustration, and the text "FlyBase Archived data files for recent releases". The navigation menu includes "Home", "Tools", "Files", "Species", "Documents", "Resources", "News", "Help", and "Archives". The "Archives" menu is open, showing options like "Help", "Open All", and "Close All".

FB2015_01, released February 24th, 2015

FlyBase Archived data files for recent releases


Home Tools Files Species Documents Resources News Help Archives Jump to Gene Go

Help Open All Close All

For items listed on FlyBase prior to October 2003 please contact FlyBase

- Previous Releases of FlyBase
- Previous Release Notes
- Main Data Archives
- Synonyms
- Genes
- Alleles and Stocks
- Human Disease
- Nomenclature
- Ontology Terms
- Genomes: Annotation and Sequence
- Transcripts and Polypeptides
- Transposons, Transgenic Constructs, and Insertions
- Aberrations
- Large Dataset Metadata
- Clones
- References
- News
- Map Conversion Tables

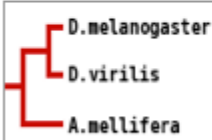



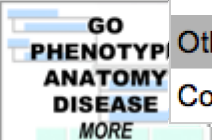


Access to Release 5 data: FlyBase Archives



FB2015_01, released February 24th, 2015

A Database of *Drosophila* Genes & Genomes

Home Tools Files Species Documents Resources News Help Archives

 BLAST	 GBrowse	 QueryBuilder	 RNA-Seq Search	 Vocabularies	 ImageBrowse	 Batch Download
--	--	---	--	---	--	---

Prior Release
Other Archives
Coordinate Converter

http://flybase.org/static_pages/downloads/archivedata3.html

Previous Releases of FlyBase		
Releases Still Active		
FB2014_06 November (Dmel Release 6.03)	GBrowse	BLAST
FB2014_04 May (Dmel Release 6.01)	GBrowse	BLAST
FB2014_03 May (Dmel Release 5.57)	GBrowse	BLAST
FB2012_06 November (Dmel Release 5.48)	GBrowse	BLAST
FB2010_07 September (Dmel Release 5.30)	GBrowse	BLAST
FB2009_09 October (Dmel Release 5.22)	GBrowse	BLAST
FB2008_09 October (Dmel Release 5.12)	GBrowse	BLAST
FB2008_07 August (Dmel Release 5.10)	GBrowse	BLAST
FB2007_01 August (Dmel Release 5.2)	GBrowse	BLAST
2006 March (Dmel Release 4.3)	GBrowse	BLAST
2004 November (Dmel Release 3.2.2)	GBrowse	BLAST
Other Releases		

GBrowse

BLAST

Access to Release 5 data: FlyBase FTP site

FB2015_01, released February 24th, 2015

FlyBase

A Database of *Drosophila* Genes & Genomes

Home Tools **Files** Species Documents Resources News Help Archives

Files Overview

Current release

Archived releases


Map Conversion

BLAST


FTP site:

Releases (FTP)

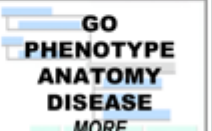
Genomes (FTP)




BeryBuilder




RNA-Seq Search



Vocabularies




ImageBrowse



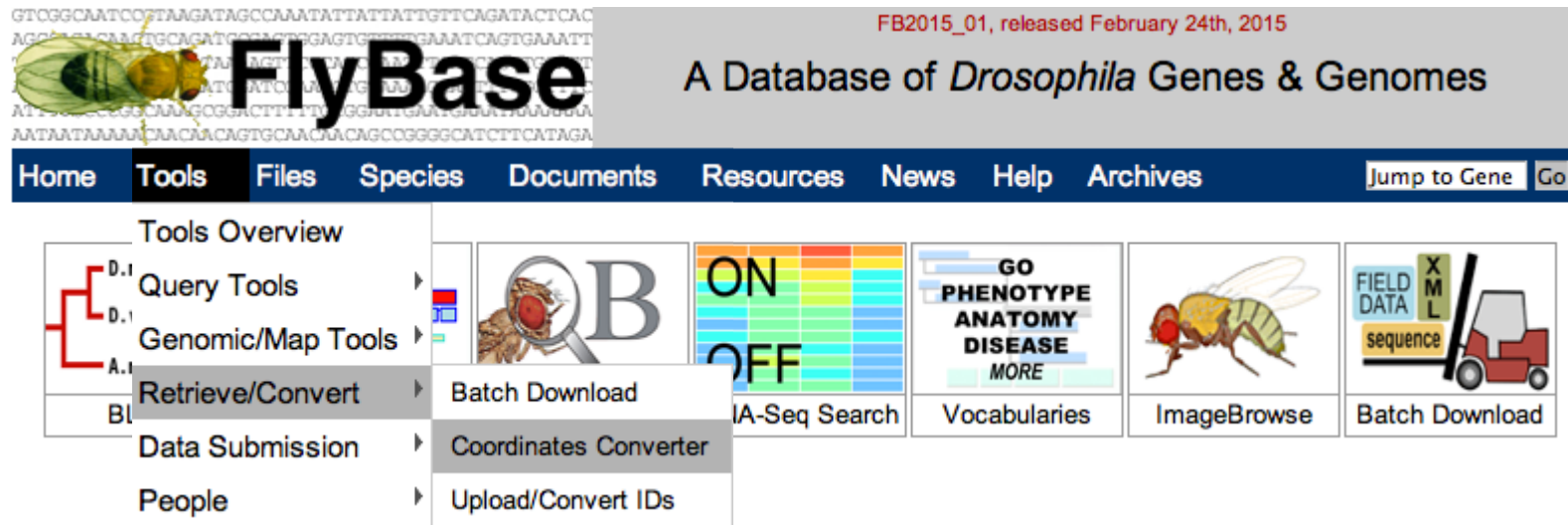
Batch Download

Index of ftp://ftp.flybase.net/releases/FB2014_03/

 [Up to higher level directory](#)

Name	Size	Last Modified
 FB2014_03		5/9/14 12:00:00 AM
 chado-xml		5/9/14 12:00:00 AM
 collaborators		5/9/14 12:00:00 AM
dana_r1.3		5/9/14 12:00:00 AM
dere_r1.3		5/9/14 12:00:00 AM
dgr1_r1.3		5/9/14 12:00:00 AM
dmel_r5.57		5/9/14 12:00:00 AM
dmoj_r1.3		5/9/14 12:00:00 AM
dper_r1.3		5/9/14 12:00:00 AM
dpse_r3.1		5/9/14 12:00:00 AM
dsec_r1.3		5/9/14 12:00:00 AM
dsim_r1.4		5/9/14 12:00:00 AM
dvir_r1.2		5/9/14 12:00:00 AM
dwil_r1.3		5/9/14 12:00:00 AM
dyak_r1.3		5/9/14 12:00:00 AM
 precomputed_files		5/9/14 12:00:00 AM
 psql		5/9/14 12:00:00 AM
 reporting-xml		5/9/14 12:00:00 AM

Coordinates Conversion: FlyBase converter



The image shows the FlyBase website header. At the top left is a fly icon. To its right is the text "FlyBase" in a large, bold font. Further right, it says "A Database of *Drosophila* Genes & Genomes". Above this text, in smaller red font, is "FB2015_01, released February 24th, 2015". Below the header is a dark blue navigation bar with white text for "Home", "Tools", "Files", "Species", "Documents", "Resources", "News", "Help", and "Archives". On the right side of this bar is a "Jump to Gene" search box with a "Go" button. A dropdown menu is open under the "Tools" tab, listing "Tools Overview", "Query Tools", "Genomic/Map Tools", "Retrieve/Convert", "Data Submission", and "People". The "Retrieve/Convert" option is highlighted, and a sub-menu is open showing "Batch Download", "Coordinates Converter", and "Upload/Convert IDs". To the right of the navigation bar are several utility icons: a magnifying glass over a fly, a heatmap, a box with "GO PHENOTYPE ANATOMY DISEASE MORE", a fly image, and a box with "FIELD DATA XML sequence" and a forklift icon.

http://flybase.org/static_pages/downloads/COORD.html

Drosophila Sequence Coordinates Converter

Species: Input Assembly: Output Assembly: Send results to:

Enter Drosophila Coordinates:

or Upload File of Coordinates:
 no file selected

Examples: 3L:18386078..18396077 or X:2684632

R6 -> R5 backwards convertor is [available here](#)

Coordinates Conversion: NCBI remap tool

<http://www.ncbi.nlm.nih.gov/genome/tools/remap#>

NCBI Resources How To

NCBI Genome Remapping Service

* indicates required fields.

Assembly-Assembly Clinical Remap Alt loci remap

Genome Information

Source Organism *	Source Assembly *	Target Assembly *
<input type="text" value="Drosophila melanogaster"/> <small>Start typing to get a list of available organisms</small>	<input type="text" value="Release 6 plus ISO1 MT"/> Release 6 plus MT Release 5	<input type="text" value="Release 6 plus ISO1 MT"/> Release 6 plus MT

Alignments performed: September 20, 2014, software version: 1.7

<u>First Pass(Reciprocal Best Hits)</u>	<u>Total</u>
Release 5 Coverage: 0.977	Release 5 Coverage: 0.980
Release 6 plus ISO1 MT Coverage: 0.952	Release 6 plus ISO1 MT Coverage: 0.974
Percent Identity: 0.999	Percent Identity: 0.999

* The Release 6 “plus MT” and “plus ISO1 MT” differ only in the mitochondrial genome.

FlyBase policy: migration of new data to Release 6

- For a limited time, FlyBase will accept Release 5-based data and lift it over to Release 6.
- FlyBase will replace any FlyBase-migrated dataset with a new analysis directly mapped to the Release 6 genome assembly.

Be mindful of the reference assembly in use

FlyBase version

Dmel Release 6 genome assembly

4th gene model annotation version on this assembly

The screenshot shows the FlyBase website interface. At the top, the FlyBase logo is displayed with a fly image. Below the logo, the text "FlyBase" is prominently shown. To the right, the text "D. melanogaster (R6.04)" is displayed, with a red bracket above it indicating the "FlyBase version" and a red arrow pointing to it from the "Dmel Release 6 genome assembly" label. Below this, a navigation bar contains links for Home, Tools, Files, Species, Documents, Resources, News, Help, and Archives. A "Jump to Gene" button is also visible. The main content area shows the gene "D. melanogaster: 13.11 kbp from 2L:7,305,159..7,318,265". Below this, there are tabs for "Browser", "Select Tracks", "Custom Tracks", and "Preferences". The "Browser" tab is active, showing a genomic track for the "wg" gene. The track includes a "Transcript" track and a "Gene Span" track. The "Gene Span" track shows the gene structure with exons and introns, and a yellow highlight is present under the gene span. The bottom of the page shows the version "version FB2015_01, released February 24, 2015" and social media icons for Twitter, YouTube, and a general social media icon.

Be mindful of the reference assembly in use

GTGGGCATCCCTAAGATAGCCAAATATTATTATTGTTTCAGATACTCAC
AGGCTGCAGGTGCGATGCGAGTGTGAGAGATCGAGTGAATTT
ATTCGCGCGGCAAGCGACTTTTGCGGTGAAAGAAATGAAATGAA
AATAATATAAAACACACAGTGCAAGCAAGCCGGGGCATCTTCATAGA

FB2015_01, released February 24th, 2015

FlyBase

A Database of *Drosophila* Genes & Genomes

Home Tools Files Species Documents Resources News Help Archives Jump to Gene Go

BLAST GBrowse Search Vocabularies ImageBrowse Batch Download

GO
PHENOTYPE
ANATOMY
DISEASE
MORE

FIELD DATA XML
sequence

Release Notes

Release notes

http://flybase.org/static_pages/docs/release_notes.html

- General FlyBase statistics.
- Detailed information about the reference genome assembly in use for each species.
- Summary statistics on gene model annotations and other annotated features.

Be mindful of the reference assembly in use

- Specify the reference assembly and FlyBase annotation version used in your publications.
- Check the reference assembly and annotation version in use at other databases, resources and datasets.

Using GBrowse 2.0 to visualize and share next-generation sequence data

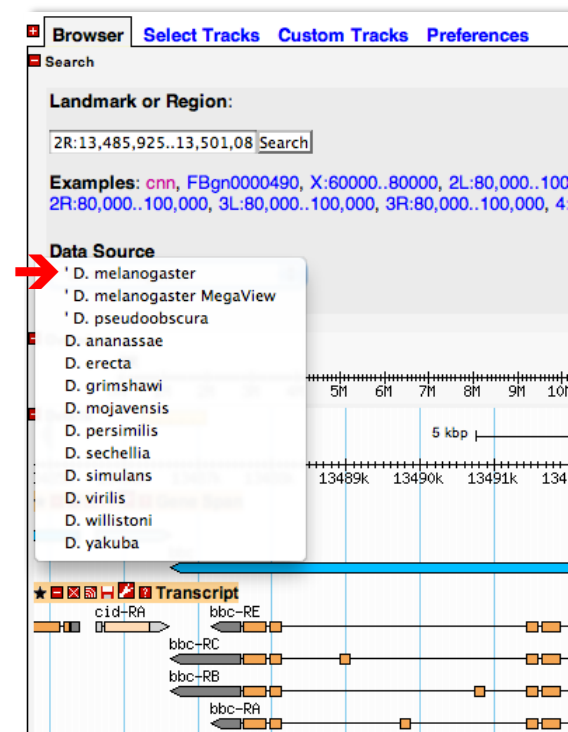
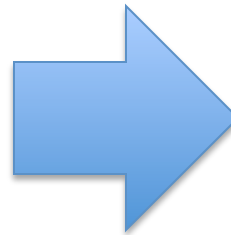
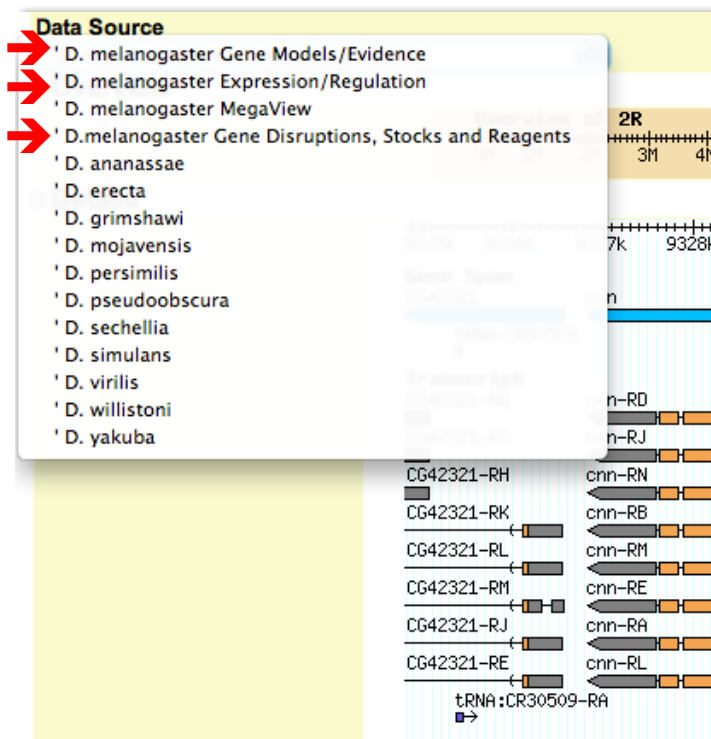
Lincoln D. Stein

Submitted: 27th September 2012; Received (in revised form): 18th December 2012

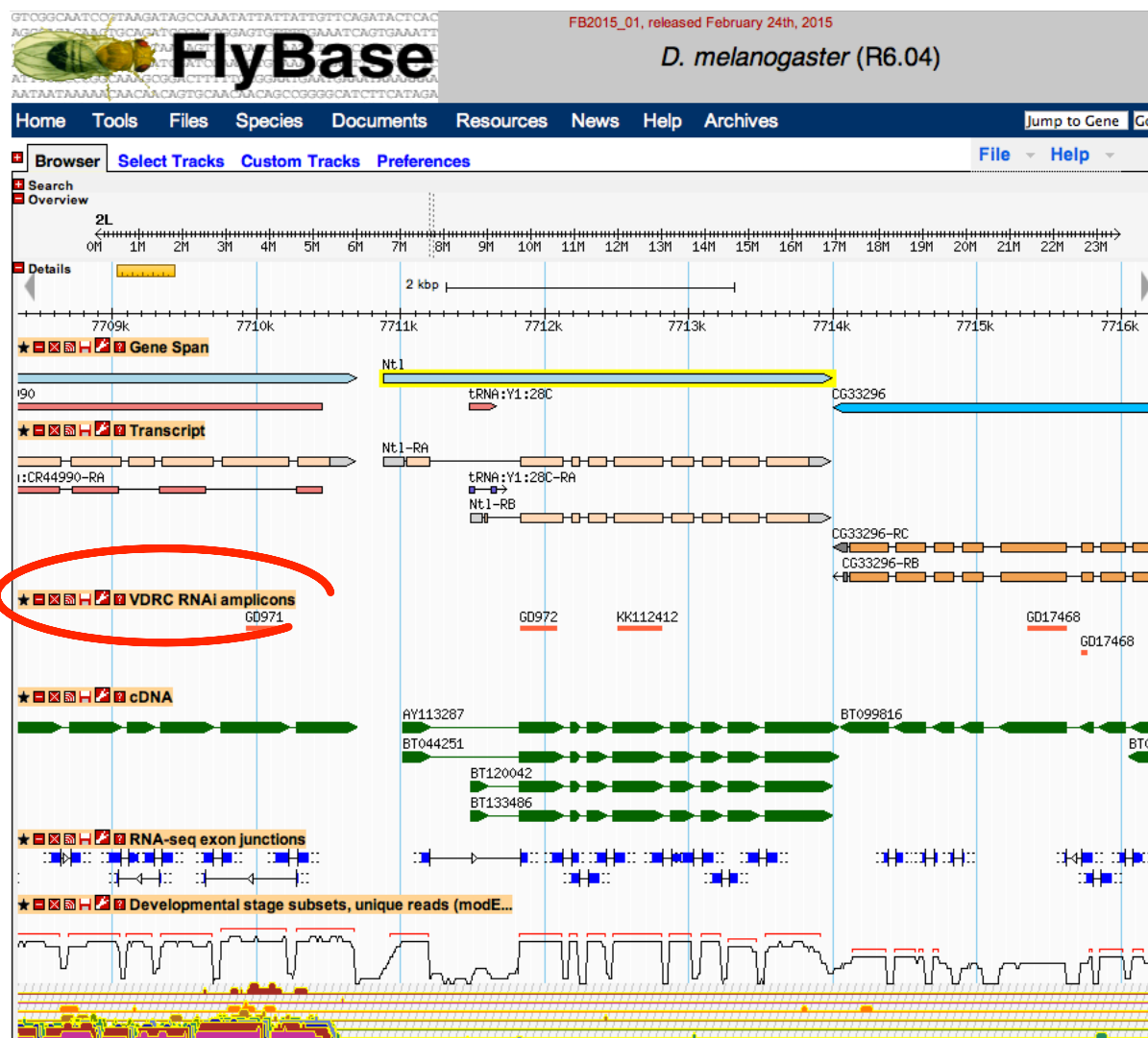
- GBrowse 2 was developed by the Generic Model Organism Database (GMOD), and integrates nicely with GMOD tools.
- GBrowse 2 (2010) replaces GBrowse (2002).
- FlyBase has offered GBrowse 2 (beta) since March 2013.

GBrowse 2 handles more data

- Display of quantitative (wiggle) tracks and next-generation sequencing (NGS) data.
- Ability to display all tracks in a single view.



GBrowse 2: easier track customization



track title
tool bar

GBrowse 2: easier track customization

The screenshot displays the FlyBase genome browser interface for *D. melanogaster* (R6.04). The top navigation bar includes links for Home, Tools, Files, Species, Documents, Resources, News, Help, and Archives, along with a "Jump to Gene" button. The main content area shows a genomic track for a region on chromosome 2L, spanning from approximately 7709k to 7716k. A 2 kbp scale bar is visible above the track. The track is divided into several sections, each with a set of control icons (star, square, magnifying glass, and a red 'X') for customization. A callout box with a hand icon points to the "VDRc RNAi amplicons" track, with the text "Turn off this track" inside. The tracks shown include: Gene Span (yellow bar), Transcript (various colored bars for Nt1, tRNA:Y1:28C, Nt1-RA, tRNA:Y1:28C-RA, Nt1-RB, CG33296, CG33296-RC, CG33296-RB, and GD17468), VDRc RNAi amplicons (red bars for GD971, GD972, KK112412, and GD17468), cDNA (green bars for AY113287, BT044251, BT120042, BT133486, BT099816, and BT06), RNA-seq exon junctions (blue bars), and Developmental stage subsets, unique reads (modE...). The bottom of the interface shows a signal plot and a heatmap.

GBrowse 2: easier track customization

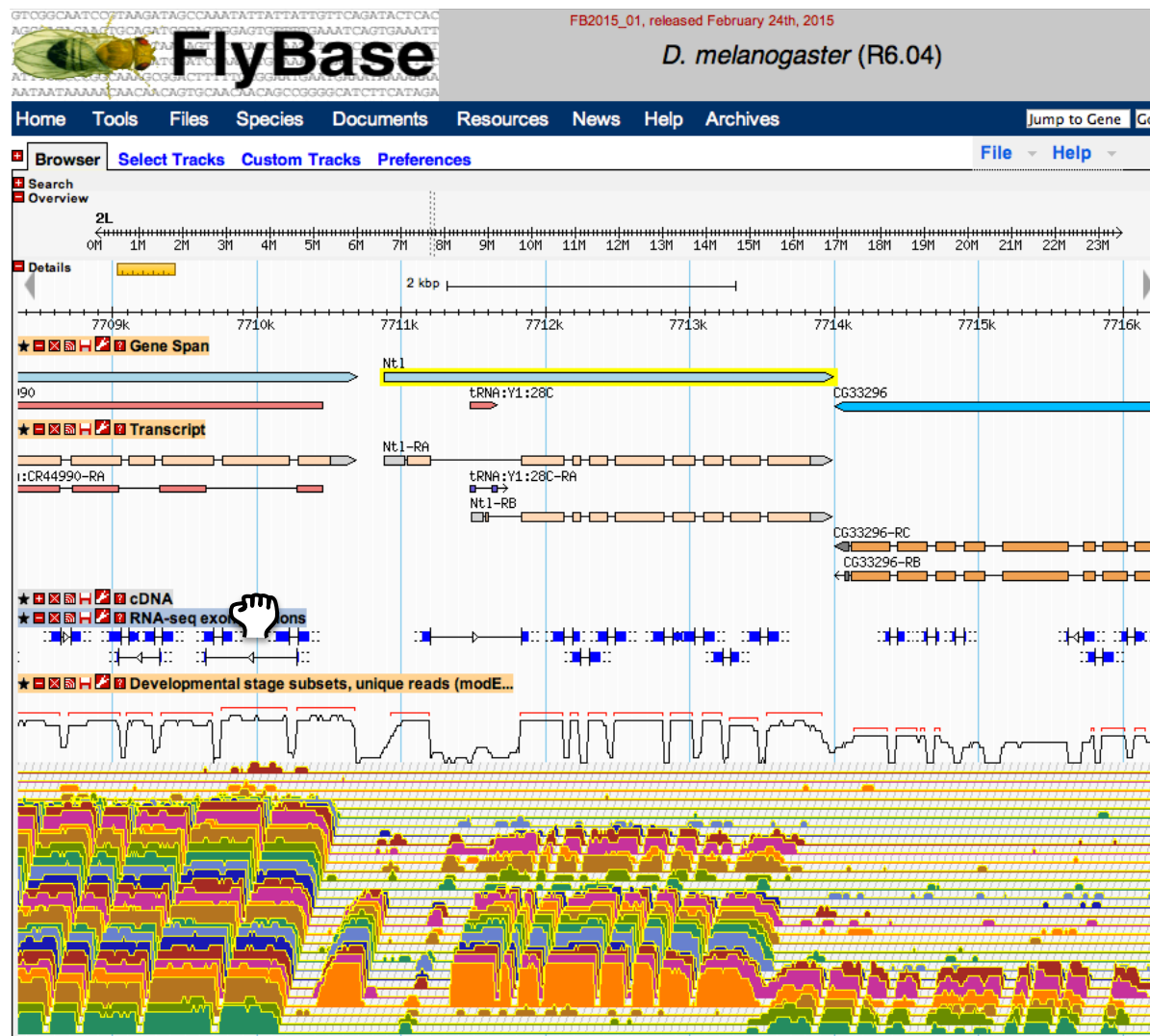
The screenshot displays the FlyBase genome browser interface for *D. melanogaster* (R6.04). The top navigation bar includes links for Home, Tools, Files, Species, Documents, Resources, News, Help, and Archives, along with a "Jump to Gene" button. The main content area shows a genomic track with various annotations. A callout box highlights the "Show or hide this track" control for the cDNA track.

Genomic Track Details:

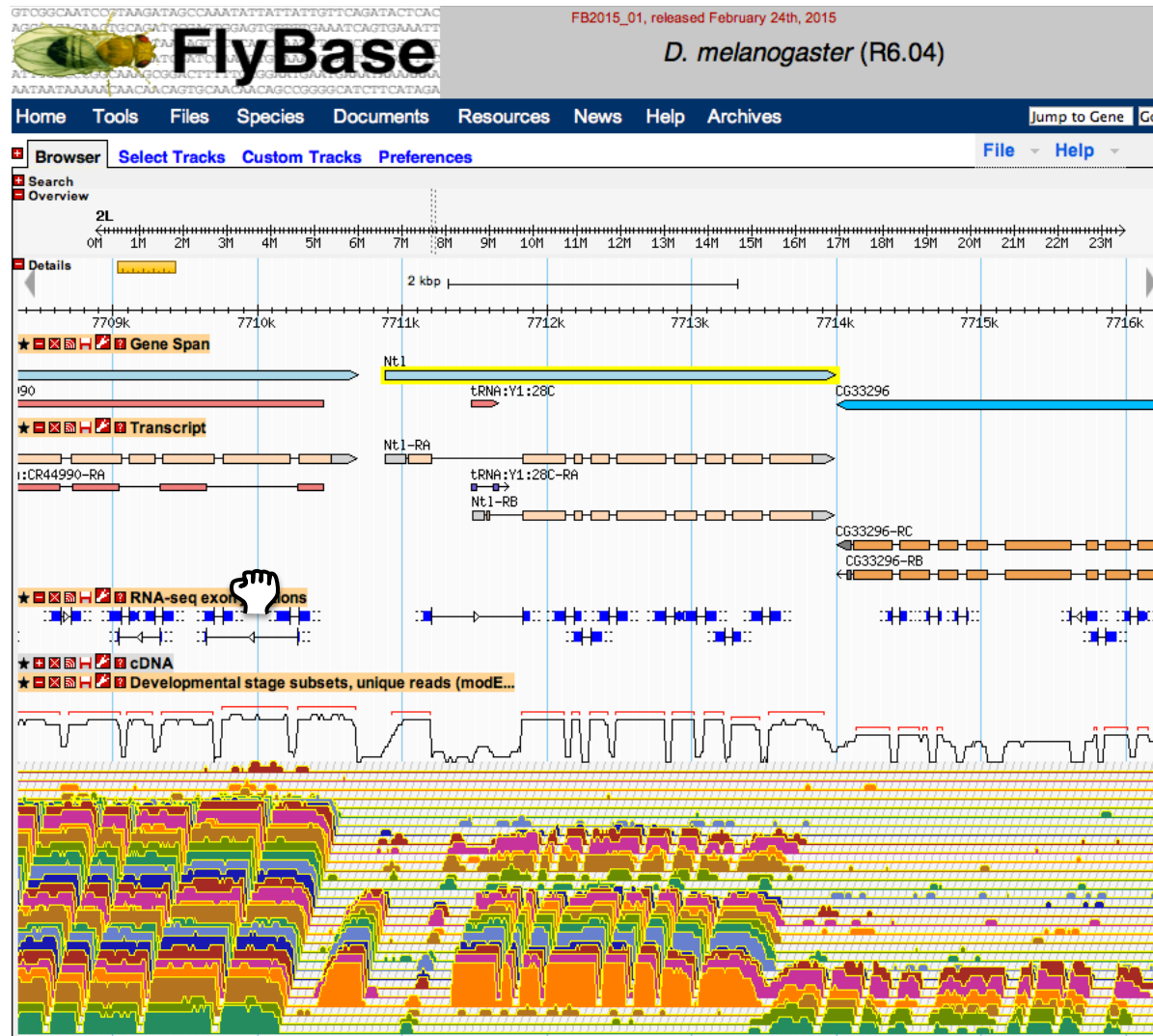
- Gene Span:** Shows the Nt1 gene structure with exons and introns.
- Transcript:** Displays various transcripts including Nt1-RA, Nt1-RB, and tRNA:Y1:28C.
- cDNA:** Shows cDNA clones such as AY113287, BT044251, BT120042, BT133486, BT099816, and BT0E.
- RNA-seq exon junctions:** Visualizes exon junctions from RNA-seq data.
- Developmental stage subsets, unique reads (modE...):** Shows developmental stage-specific expression patterns.

Callout Box: A speech bubble with a hand icon pointing to the cDNA track control, containing the text "Show or hide this track".

GBrowse 2: easier track customization



GBrowse 2: easier track customization

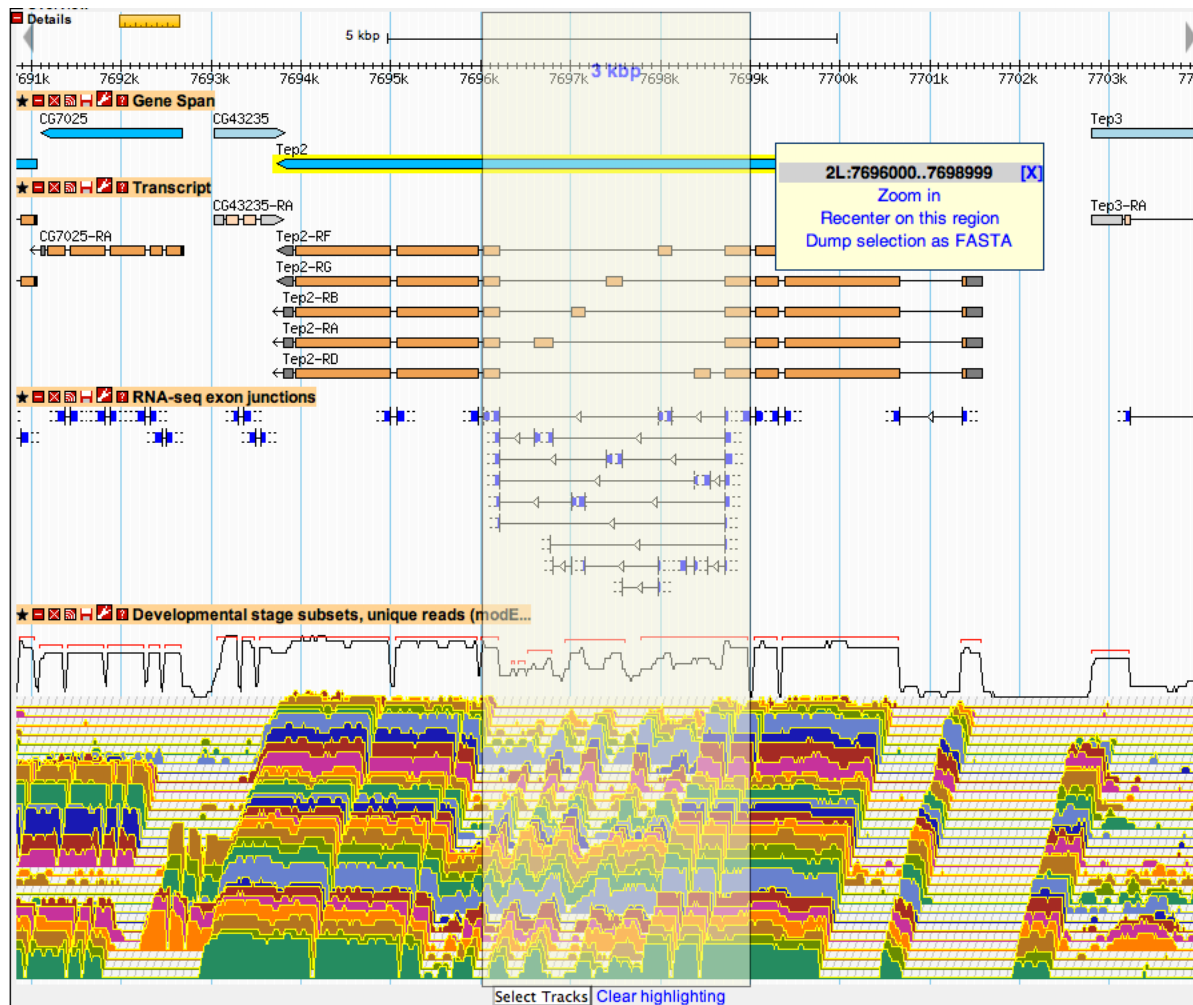


GBrowse 2: click-and-drag zoom



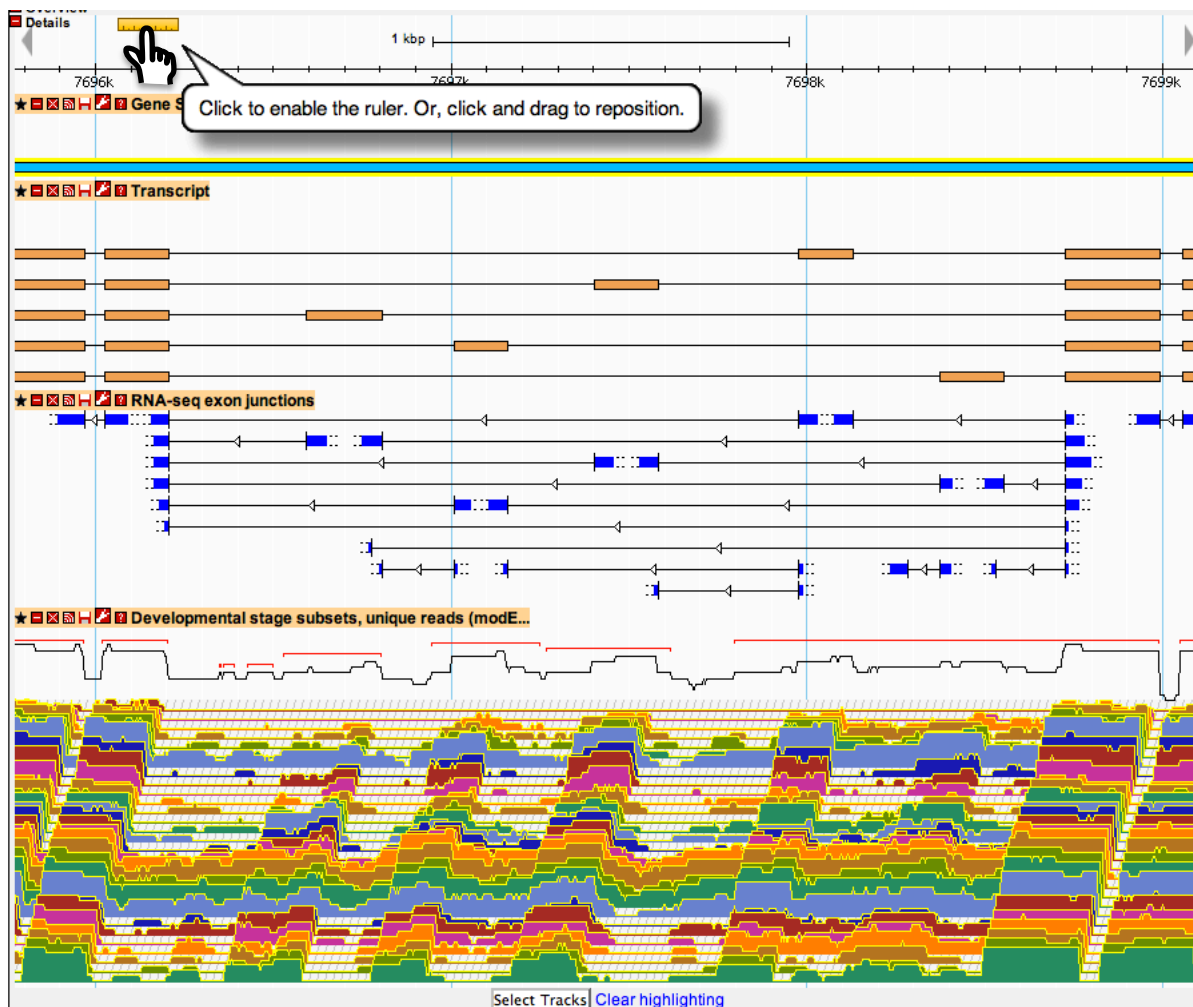
click-and-drag
selection

GBrowse 2: click-and-drag zoom



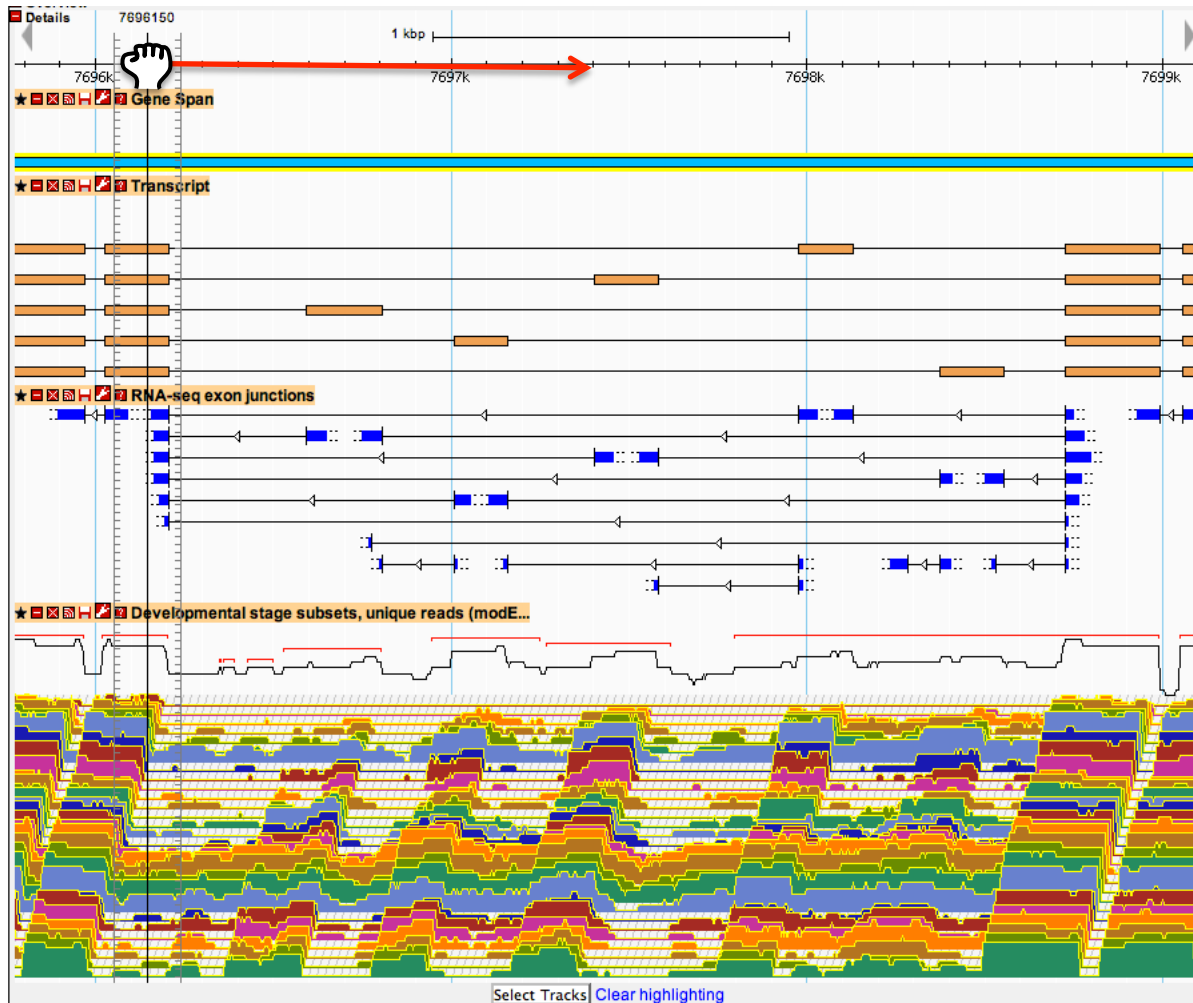
GBrowse 2: ruler

click on ruler

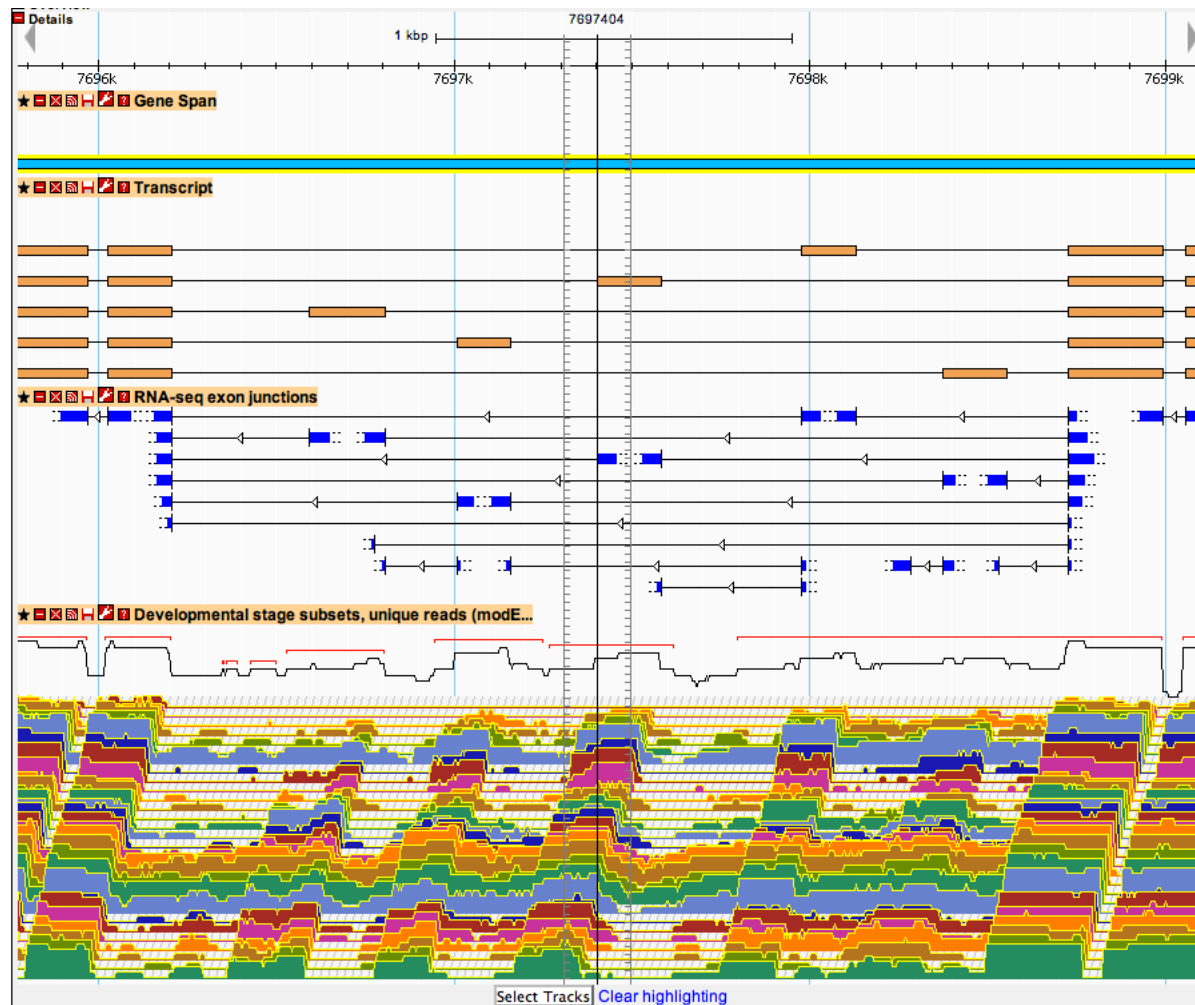


GBrowse 2: ruler

drag ruler

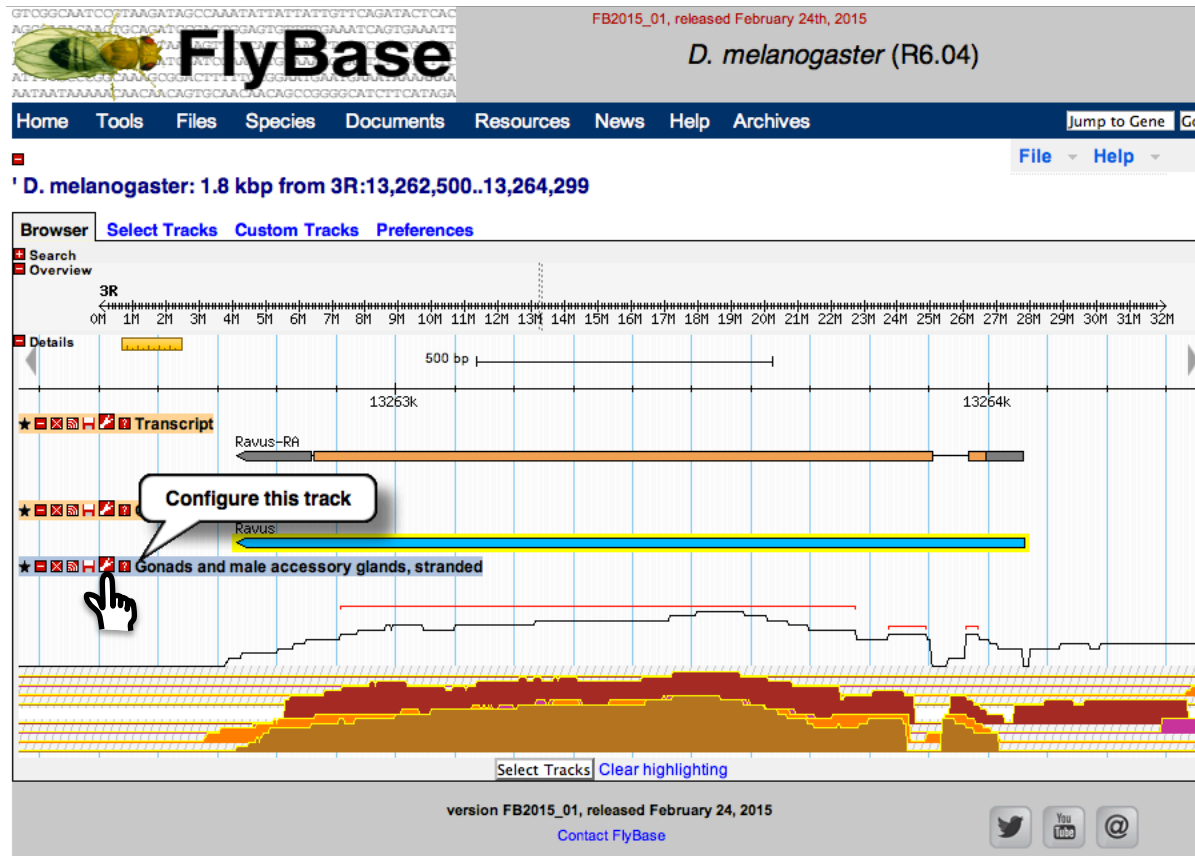


GBrowse 2: ruler



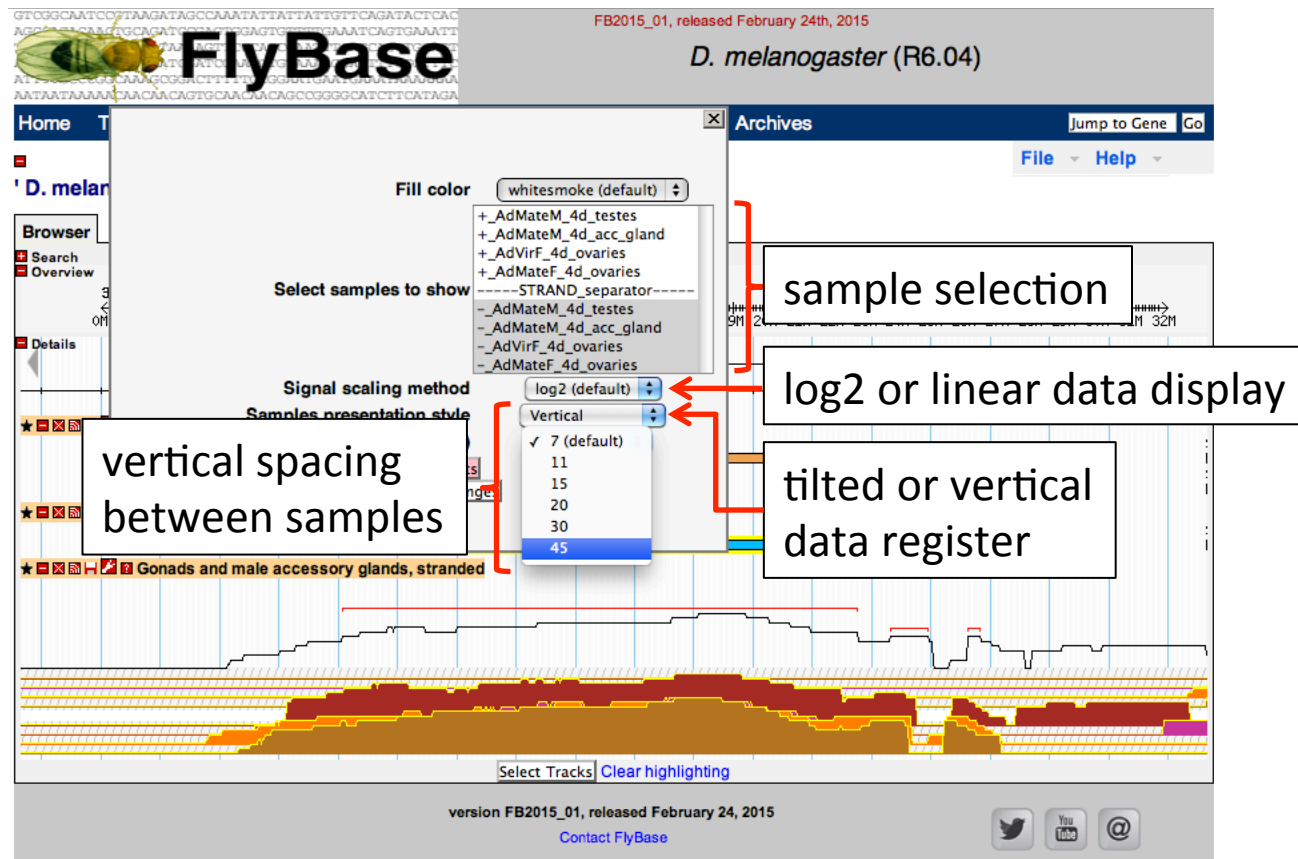
New RNA-Seq display options: sample selection

 track configuration icon (wrench)

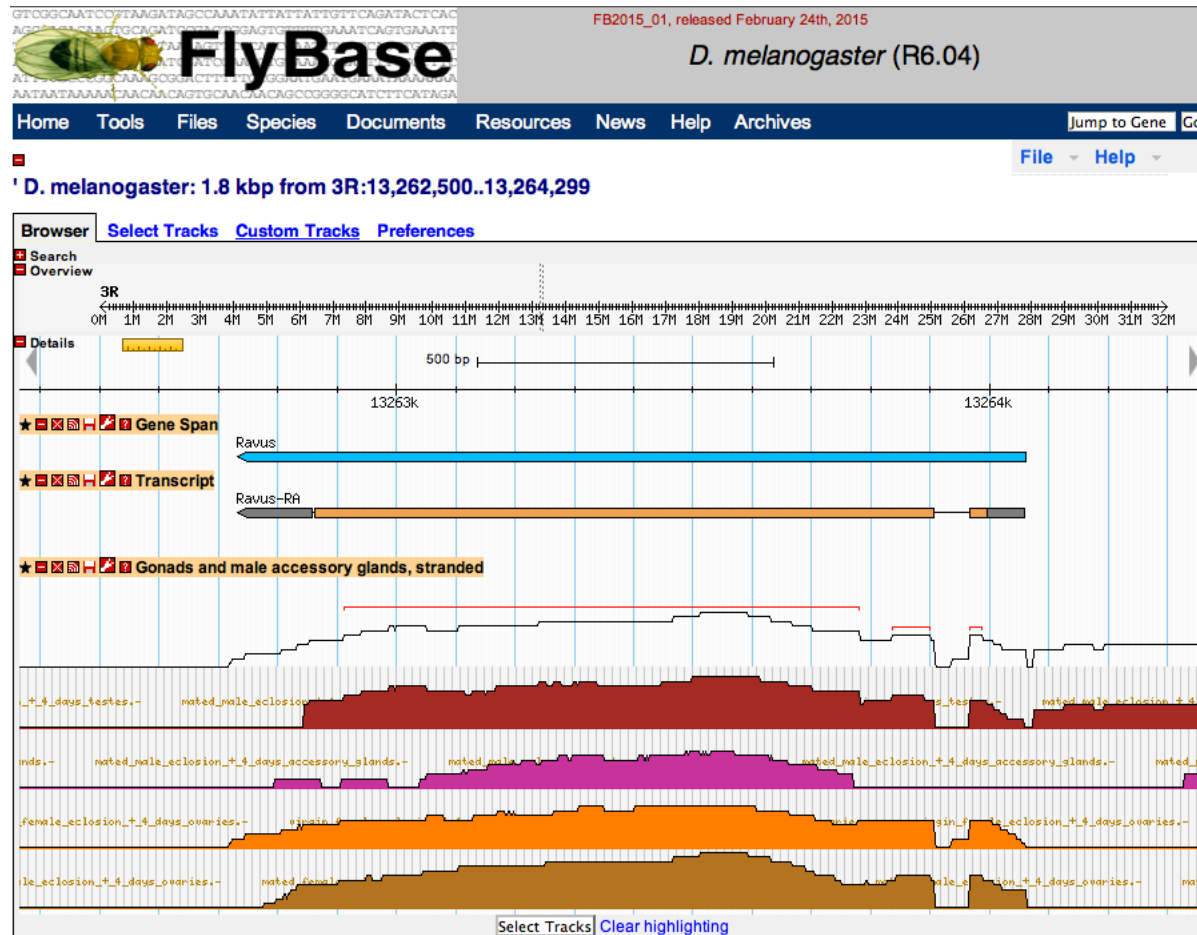


The screenshot displays the FlyBase genome browser interface for *D. melanogaster* (R6.04). The main content area shows a genomic region from 13,262,500 to 13,264,299 bp on chromosome 3R. Several tracks are visible, including a 'Transcript' track with 'Ravus-RA' and 'Ravus' transcripts, and a 'Gonads and male accessory glands, stranded' track. A callout box labeled 'Configure this track' points to the wrench icon in the track configuration menu for the 'Gonads and male accessory glands, stranded' track. The interface includes a navigation bar with 'Home', 'Tools', 'Files', 'Species', 'Documents', 'Resources', 'News', 'Help', and 'Archives'. The footer shows the version 'FB2015_01, released February 24, 2015' and social media icons for Twitter, YouTube, and a general contact icon.

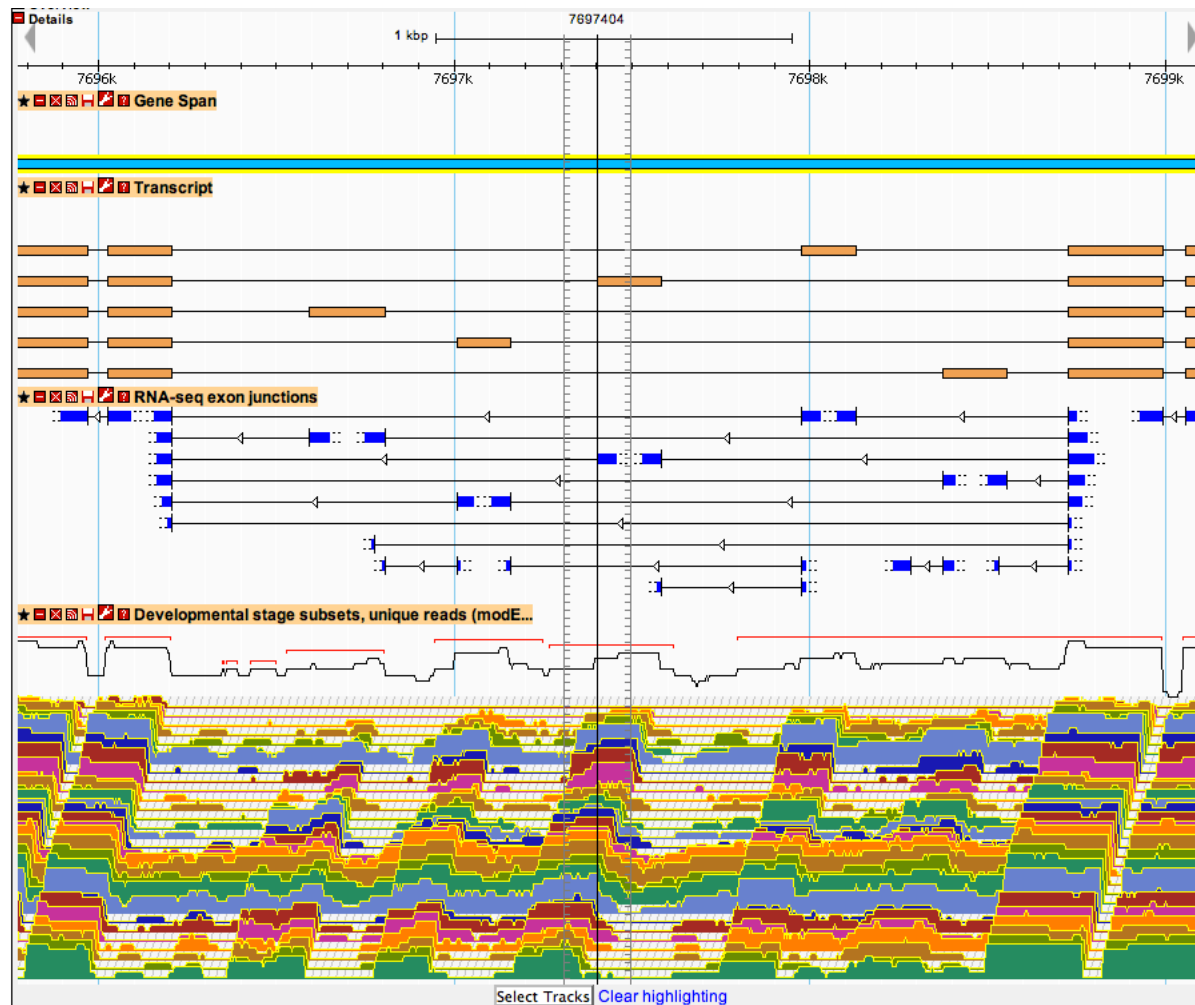
New RNA-Seq display options: sample selection



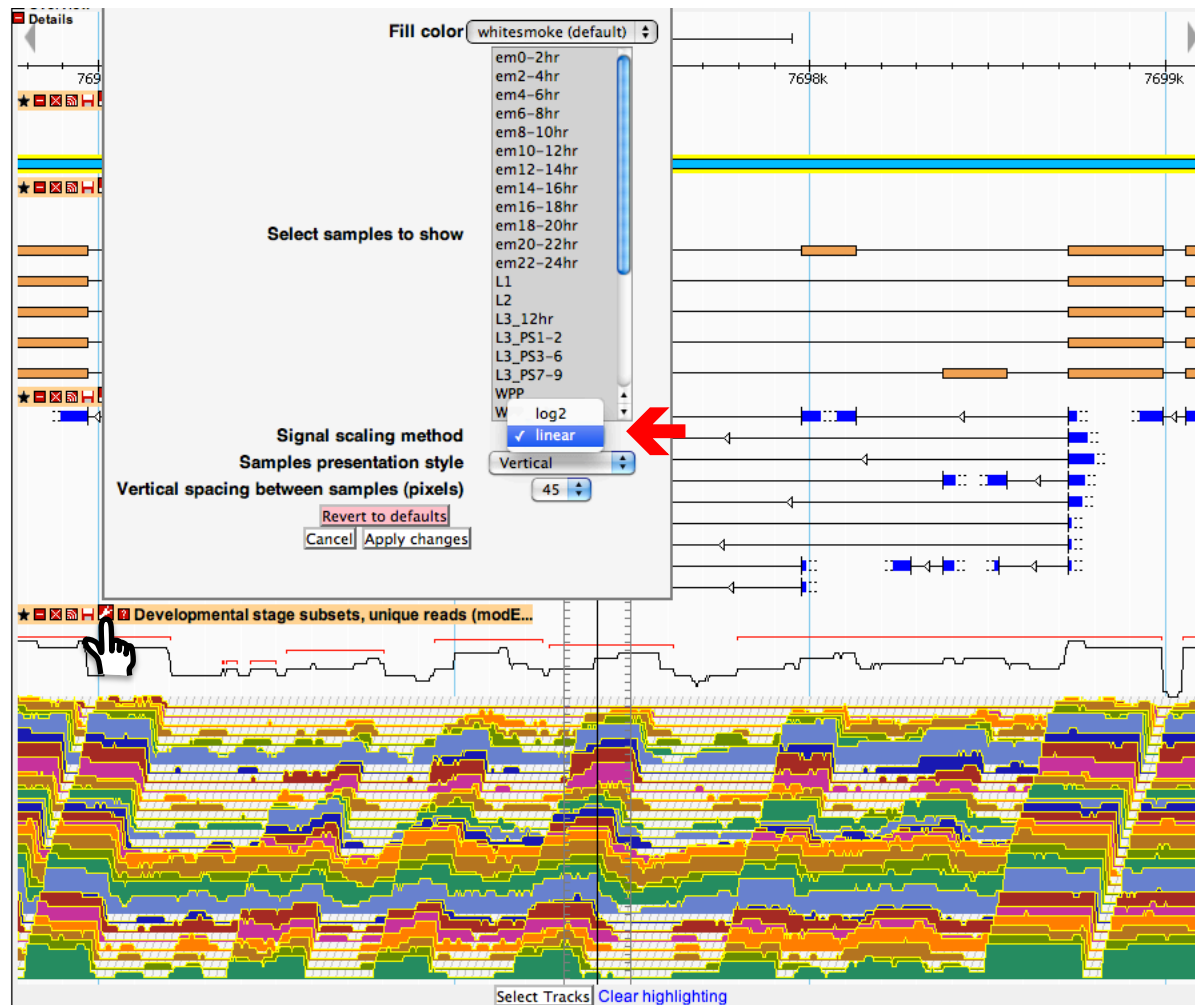
New RNA-Seq display options: sample selection



New RNA-Seq display options: linear vs. log2

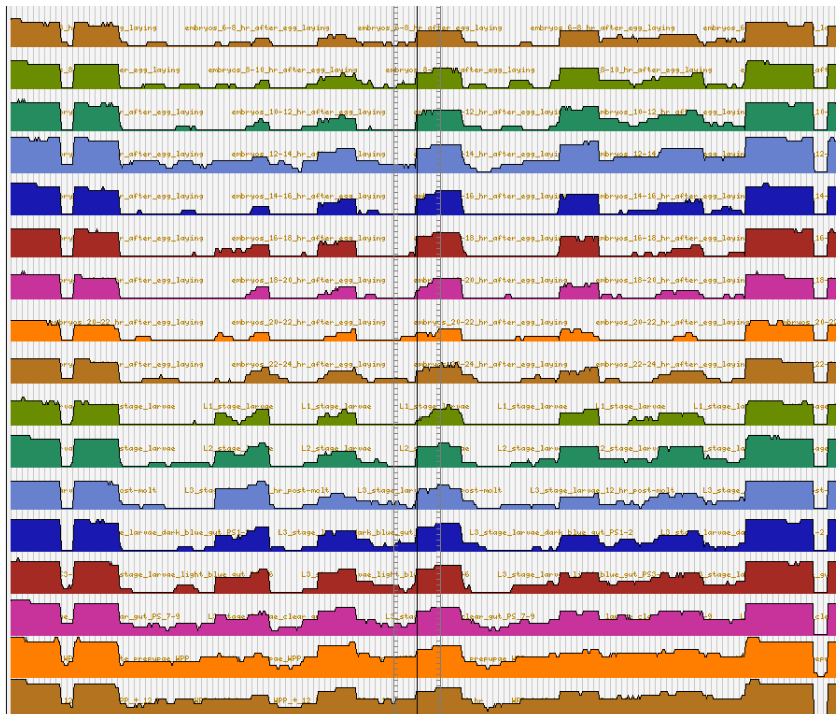


New RNA-Seq display options: linear vs. log2

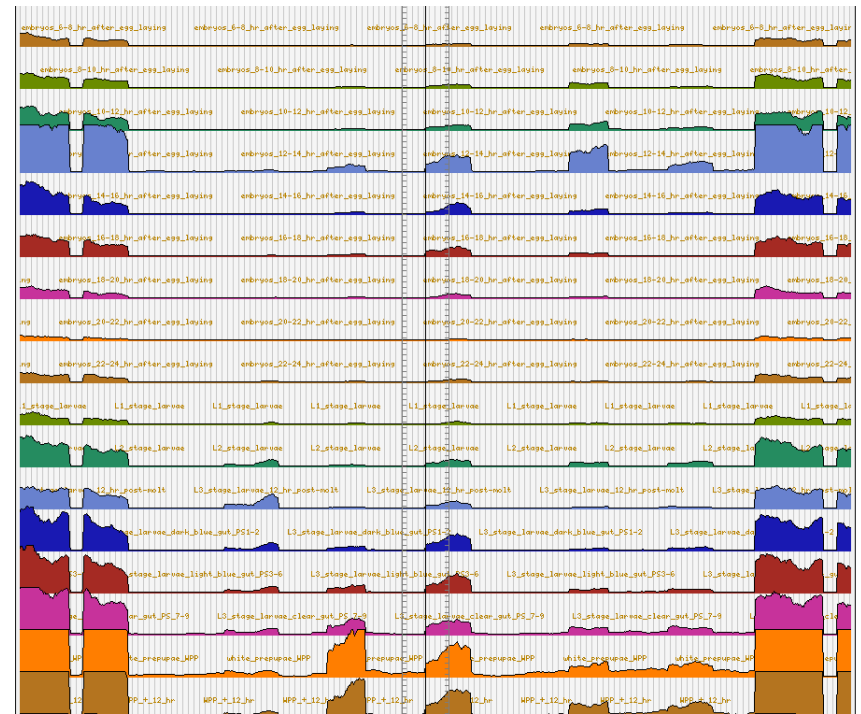


New RNA-Seq display options: linear vs. log2

log2 scale



linear scale



Sequence download: decorated FASTA

FB2015_01, released February 24th, 2015

FlyBase *D. melanogaster* (R6.04)

Home Tools Files Species Documents Resources News Help Archives [Jump to Gene](#) [Go](#)

[File](#) [Help](#)

' *D. melanogaster*: 2.8 kbp from 3R:5,791,700..5,794,499

Browser [Select Tracks](#) [Custom Tracks](#) [Preferences](#)

Search

Landmark or Region:
3R:5,791,700..5,794,499 [Search](#)

Examples: [cnn](#), [FBgn0000490](#), [X:60000..80000](#), [2L:80,000..100,000](#), [2R:80,000..100,000](#), [3L:80,000..100,000](#), [3R:80,000..100,000](#), [4:20000..50000](#)

Data Source
' *D. melanogaster*

Scroll/Zoom: [<<](#) [<](#) [-](#) [+](#) [>](#) [>>](#) Show 2.8 kbp

[Annotate Restriction Sites](#)
 [Download Decorated FASTA File](#) [Configure...](#) [Go](#)
[Download GFF File](#)
[Download HTML table view](#)
[Download Sequence File](#)

step 1 – choose option and hit configure

[Configure... Decorated FASTA File](#)

The marked-up FASTA dumper plugin dumps out the currently displayed genomic segment in FASTA format.
This plugin was written by Lincoln Stein and Jason Stajich.

[Cancel](#) [Configure](#) [Go](#)

Output text html
Orientation Flip
Gene Span None CAPS Bold Underline Italics Font red Bkg red
Transcript None CAPS Bold Underline Italics Font red Bkg red
CDS None CAPS Bold Underline Italics Font red Bkg green

[Cancel](#) [Configure](#) [Go](#)

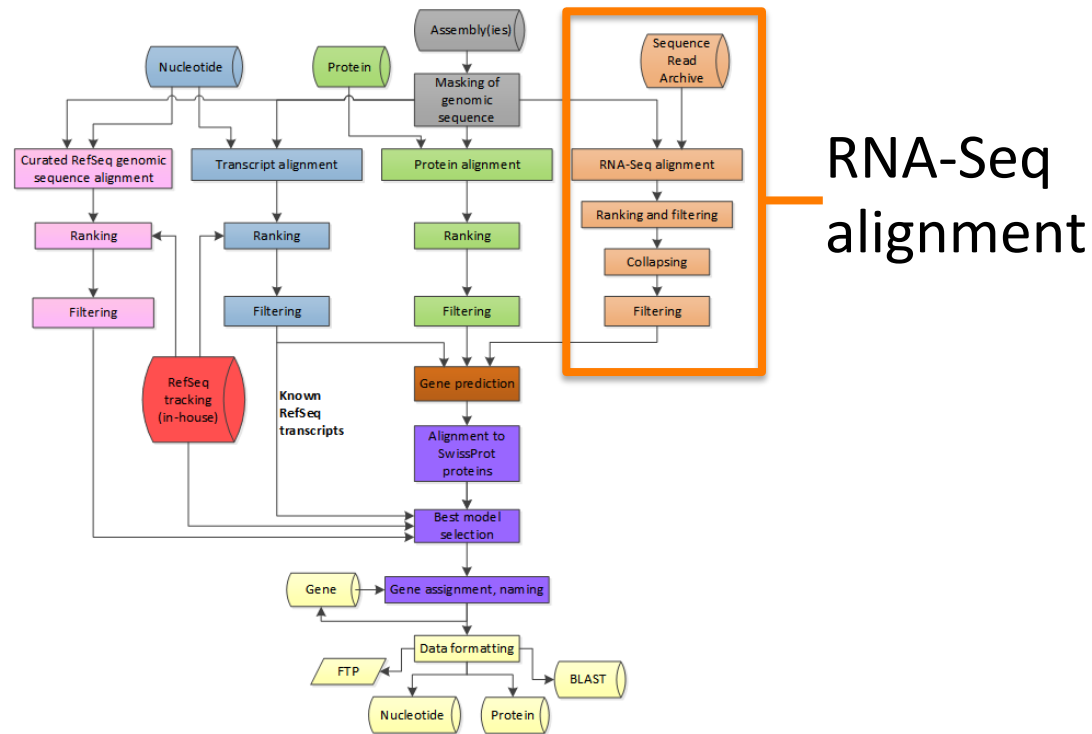
step 2 – choose options

step 3 – hit go

Sequence download: decorated FASTA

```
>3R:5791700..5794499
actaaaattgaatttaagtgccaataaaagtatacaagtttatgaaaagtttattagot
tttcaccaaggggaaatgtctgggctgtagtatatagtgtagtattttctattaccagc
tgtcatggtaaagtatTTTTCTCAAATGGTcagaatcatcccccttgcaactttaaCG
CGTCACTGGATGCTTGTATTCTTGTAAATTTGTGCCATAGCAAACCTCACATTTTGCAAA
TTTGTTTGAAATCGGTATTGTGTACTTAAGA.TGCCAAAACAAGATTGCAAAATACG
GATAAGTGCTATCAGCAGAAATCCCGCACATTTGTCCAAATACAAATCATCCGAAAAAGCA
CAAGAACACCGAACTGGACGGCCAGAAAGCCAAAAAAGTGGCGCCAAAAAGAAAGTCAATCC
TCGCAGTCTGGTGAACAGAAAAAGGAAGAACAAACGGAGCCGGTGAACAAGGATAAGTCC
AATACGACTGCTTCAAGTACCGAGATGGTCAACAAGGATACAGCCAAAGGCCAGTTATGAA
GCCGAAACCGAGGAGCTTCACAAAGAGGCCATGAGCAACATATCCGGAAAGAACTACATG
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```

Other new stuff at FlyBase: NCBI GNOMON annotations for Drosophila



GNOMON annotations have replaced CAF1 (2006) annotations for *D. simulans*, *D. pseudoobscura*, *D. erecta*, *D. ananassae* and *D. yakuba* (more on the way).

http://www.ncbi.nlm.nih.gov/genome/annotation_euk/process/

Other new stuff at FlyBase: a new *D. simulans* genome assembly

FB2015_01, released February 24th, 2015
D. simulans (R2.01)

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D. simulans: 35.24 kbp from Scf_2L:2,294,645..2,329,881

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10 kbp

2300k 2310k 2320k 2330k

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26804

m\GD23154

Dsim\GD29003 Dsim\GD22836 Dsim\GD23155 Dsim\GD28814 Dsim\dpp

Dsim\GD22835 Dsim\GD17823 Dsim\GD22834

★ Transcript

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sim\GD23154-RA

Dsim\GD29003-RB Dsim\GD29003-RA

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For more information:

http://flybase.org/static_pages/feature/previous/articles/2015_02/Dsim_r2.01.html

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GTGGGCAATCCCTAAGATAGCCAAATATTATTATTGTTTCAGATACTCAC
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